0500/0280

OIPE

#2

RAW SEQUENCE LISTING   DATE: 10/18/2001
PATENT APPLICATION: US/09/964,412   TIME: 09:43:56

Input Set : A:\ES.txt
Output Set: N:\CRF3\10182001\I964412.raw

ENTERED

SEQUENCE LISTING
```
 4 (1) GENERAL INFORMATION:
 6        (i) APPLICANT: de la Monte, Suzanne
 7                       Wands, Jack R.
 9      (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
10                       Screening Drugs Effective for the Treatment or Prevention
11                       of Alzheimer's Disease
13     (iii) NUMBER OF SEQUENCES: 14
15      (iv) CORRESPONDENCE ADDRESS:
16            (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
17            (B) STREET: 1100 New York Ave., Suite 600
18            (C) CITY: Washington
19            (D) STATE: DC
20            (E) COUNTRY: USA
21            (F) ZIP: 20005-3934
23       (v) COMPUTER READABLE FORM:
24            (A) MEDIUM TYPE: Floppy disk
25            (B) COMPUTER: IBM PC compatible
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29      (vi) CURRENT APPLICATION DATA:
C--> 30       (A) APPLICATION NUMBER: US/09/964,412
C--> 31       (B) FILING DATE: 28-Sep-2001.
32            (C) CLASSIFICATION:
34    (viii) ATTORNEY/AGENT INFORMATION:
35            (A) NAME: Esmond, Robert W.
36            (B) REGISTRATION NUMBER: 32,893
37            (C) REFERENCE/DOCKET NUMBER: 0609.4370000
39      (ix) TELECOMMUNICATION INFORMATION:
40            (A) TELEPHONE: 202-371-2600
41            (B) TELEFAX: 202-371-2540
44 (2) INFORMATION FOR SEQ ID NO: 1:
46        (i) SEQUENCE CHARACTERISTICS:
47            (A) LENGTH: 1442 base pairs
48            (B) TYPE: nucleic acid
49            (C) STRANDEDNESS: double
50            (D) TOPOLOGY: both
52       (ii) MOLECULE TYPE: cDNA
55       (ix) FEATURE:
56            (A) NAME/KEY: CDS
57            (B) LOCATION: 15..1139
61       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC        50
64                 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
65                  1               5                  10
67 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC        98
68 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
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69          15                    20                    25
71 GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC      146
72 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
73       30                    35                    40
75 ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT      194
76 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
77 ·45                    50                    55                    60
79 CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC      242
80 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
81             65                    70                    75
83 TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC      290
84 Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
85             80                    85                    90
87 CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG      338
88 Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
89             95                    100                   105
91 TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC      386
92 Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
93       110                   115                   120
95 CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT      434
96 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
97 125                   130                   135                   140
99 TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG      482
100 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
101                   145                   150                   155
103 CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG      530
104 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
105                   160                   165                   170
107 CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC      578
108 His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
109             175                   180                   185
111 CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG      626
112 His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
113       190                   195                   200
115 AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC      674
116 Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
119 205                   210                   215                   220
121 TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC      722
122 Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
123                   225                   230                   235
125 CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT      770
126 Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
127             240                   245                   250
129 TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC      818
130 Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile
131             255                   260                   265
133 TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT      866
134 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
135       270                   275                   280
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137 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT        914
138 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
139 285                 290                 295                 300
141 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG        962
142 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
143                 305                 310                 315
145 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC        1010
146 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
147                 320                 325                 330
149 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA        1058
150 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
151           335                 340                 345
153 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT        1106
154 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
155       350                 355                 360
157 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT      1159
158 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
159 365                 370                 375
161 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA      1219
163 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT      1279
165 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTA AACAGTTACA       1339
167 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA      1399
169 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA                        1442
172 (2) INFORMATION FOR SEQ ID NO: 2:
174       (i) SEQUENCE CHARACTERISTICS:
175           (A) LENGTH: 375 amino acids
178           (B) TYPE: amino acid
179           (D) TOPOLOGY: linear
181       (ii) MOLECULE TYPE: protein
183       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
185 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
186   1               5                 10                  15
188 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
189             20                  25                  30
191 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
192           35                  40                  45
194 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
195      50                  55                  60
197 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
198 65                  70                  75                  80
200 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
201                 85                  90                  95
203 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
204             100                 105                 110
206 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
207         115                 120                 125
209 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
210     130                 135                 140
212 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
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```
213 145                 150                 155                 160
215 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
216                 165             170             175
218 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
219                 180             185             190
221 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
222         195             200             205
224 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
225     210             215             220
227 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
228 225             230             235             240
230 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
231             245             250             255
233 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
234             260             265             270
237 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
238         275             280             285
240 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
241     290             295             300
243 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
244 305             310             315             320
246 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
247             325             330             335
249 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
250         340             345             350
252 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
253         355             360             365
255 Ser Gln Thr Pro Asp Leu Arg
256     370             375
258 (2) INFORMATION FOR SEQ ID NO: 3:
260       (i) SEQUENCE CHARACTERISTICS:
261             (A) LENGTH: 1381 base pairs
262             (B) TYPE: nucleic acid
263             (C) STRANDEDNESS: double
264             (D) TOPOLOGY: both
266       (ii) MOLECULE TYPE: cDNA
271       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
273 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT    60
275 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC   120
277 AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA   180
279 GAGATGGAGT TTAACTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC   240
281 TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC   300
283 TGCCTGGCTA ATTTTTGTGG TAGAAACAGG GTTTCACTGA TGTTGCCCAA GCTGGTCTCC   360
285 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC   420
287 GTGCCTGGCC TTTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT   480
289 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC   540
291 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT   600
293 TTTATTTTTA TTTTTAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC   660
296 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC   720
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Output Set: N:\CRF3\10182001\I964412.raw

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298 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT      780
300 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT      840
302 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC      900
304 CTATTTTTAA TTTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC      960
306 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC     1020
308 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT     1080
310 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACTCCTGA CCTCAGGTGA     1140
312 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC     1200
314 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC     1260
316 TCAAACTTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT     1320
318 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA     1380
320 C                                                                     1381
322 (2) INFORMATION FOR SEQ ID NO: 4:
324      (i) SEQUENCE CHARACTERISTICS:
325          (A) LENGTH: 1418 base pairs
326          (B) TYPE: nucleic acid
327          (C) STRANDEDNESS: both
328          (D) TOPOLOGY: both
330      (ii) MOLECULE TYPE: cDNA
335      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
337 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT       60
339 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC      120
341 AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT      180
343 AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT      240
345 CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT      300
347 GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT      360
349 CAAGCAGTCC ACCTGCCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC      420
351 TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT      480
355 GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC      540
357 TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTAT      600
359 TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG      660
361 GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG      720
363 CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT      780
365 AGTAGAGATG GGGTTTCACC ATGTTCGCCA GGTTGATGCT AGATCTCTTG ACCTTGTGAT      840
367 CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC      900
369 TATTTTTAAT TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA      960
371 ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT     1020
373 CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCCGCTAA TTTTTGTATT     1080
375 TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACTCC TGACCTCAGG     1140
377 TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC     1200
379 CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG     1260
381 GTCTCAAACT TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC     1320
383 ATTTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG     1380
385 AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT                             1418
387 (2) INFORMATION FOR SEQ ID NO: 5:
389      (i) SEQUENCE CHARACTERISTICS:
390          (A) LENGTH: 22 base pairs
391          (B) TYPE: nucleic acid
392          (C) STRANDEDNESS: single
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VERIFICATION SUMMARY   DATE: 10/18/2001
PATENT APPLICATION: **US/09/964,412**   TIME: 09:43:57

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\10182001\I964412.raw**

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]